

RAW SEQUENCE LISTING

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Application Serial Number: 10/535,042
Source: PCT
Date Processed by STIC: 03/03/2006

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RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/10/535,042

TIME: 14:26:46

Input Set : A:\SALK3140.APP

Output Set: N:\CRF4\03032006\J535042.raw

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3 <110> APPLICANT: DOWNES, MICHAEL R.
4   VERDICIA, MARK A.
5   NOEL, JOSEPH P.
6   EVANS, RONALD M.
7   BOWMAN, LINDSEY J.
8   BOWMAN, MARIANNE
10 <120> TITLE OF INVENTION: STRUCTURE OF THE FARNESOID X RECEPTOR LIGAND BINDING
11   DOMAIN AND METHODS OF USE THEREFOR
13 <130> FILE REFERENCE: SALK3140-1
15 <140> CURRENT APPLICATION NUMBER: 10/535,042
16 <141> CURRENT FILING DATE: 2005-05-13
18 <150> PRIOR APPLICATION NUMBER: PCT/US03/036548
19 <151> PRIOR FILING DATE: 2003-11-14
21 <150> PRIOR APPLICATION NUMBER: 60/426,665
22 <151> PRIOR FILING DATE: 2002-11-15
24 <150> PRIOR APPLICATION NUMBER: 60/426,668
25 <151> PRIOR FILING DATE: 2002-11-15
27 <160> NUMBER OF SEQ ID NOS: 6
29 <170> SOFTWARE: PatentIn Ver. 3.3
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 476
33 <212> TYPE: PRT
34 <213> ORGANISM: Homo sapiens
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40 Asp Glu Phe Ser Phe Ser Glu Asn Leu Phe Gly Val Leu Thr Glu Gln
41   20           25           30
43 Val Ala Gly Pro Leu Gly Gln Asn Leu Glu Val Glu Pro Tyr Ser Gln
44   35           40           45
46 Tyr Ser Asn Val Gln Phe Pro Gln Val Gln Pro Gln Ile Ser Ser Ser
47   50           55           60
49 Ser Tyr Tyr Ser Asn Leu Gly Phe Tyr Pro Gln Gln Pro Glu Glu Trp
50   65           70           75           80
52 Tyr Ser Pro Gly Ile Tyr Glu Leu Arg Arg Met Pro Ala Glu Thr Leu
53   85           90           95
55 Tyr Gln Gly Glu Thr Glu Val Ala Glu Met Pro Val Thr Lys Lys Pro
56   100          105          110
58 Arg Met Gly Ala Ser Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val
59   115          120          125
61 Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys
62   130          135          140
64 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val

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65 145          150          155          160
67 Tyr Lys Cys Lys Asn Gly Gly Asn Cys Val Met Asp Met Tyr Met Arg
68          165          170          175
70 Arg Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Lys Glu Met Gly Met
71          180          185          190
73 Leu Ala Glu Cys Met Tyr Thr Gly Leu Leu Thr Glu Ile Gln Cys Lys
74          195          200          205
76 Ser Lys Arg Leu Arg Lys Asn Val Lys Gln His Ala Asp Gln Thr Val
77          210          215          220
79 Asn Glu Asp Ser Glu Gly Arg Asp Leu Arg Gln Val Thr Ser Thr Thr
80 225          230          235          240
82 Lys Ser Cys Arg Glu Lys Thr Glu Leu Thr Pro Asp Gln Gln Thr Leu
83          245          250          255
85 Leu His Phe Ile Met Asp Ser Tyr Asn Lys Gln Arg Met Pro Gln Glu
86          260          265          270
88 Ile Thr Asn Lys Ile Leu Lys Glu Glu Phe Ser Ala Glu Glu Asn Phe
89          275          280          285
91 Leu Ile Leu Thr Glu Met Ala Thr Asn His Val Gln Val Leu Val Glu
92          290          295          300
94 Phe Thr Lys Lys Leu Pro Gly Phe Gln Thr Leu Asp His Glu Asp Gln
95 305          310          315          320
97 Ile Ala Leu Leu Lys Gly Ser Ala Val Glu Ala Met Phe Leu Arg Ser
98          325          330          335
100 Ala Glu Ile Phe Asn Lys Lys Leu Pro Ser Gly His Ser Asp Leu Leu
101          340          345          350
103 Glu Glu Arg Ile Arg Asn Ser Gly Ile Ser Asp Glu Tyr Ile Thr Pro
104          355          360          365
106 Met Phe Ser Phe Tyr Lys Ser Ile Gly Glu Leu Lys Met Thr Gln Glu
107          370          375          380
109 Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Leu Ser Pro Asp Arg Gln
110 385          390          395          400
112 Tyr Ile Lys Asp Arg Glu Ala Val Glu Lys Leu Gln Glu Pro Leu Leu
113          405          410          415
115 Asp Val Leu Gln Lys Leu Cys Lys Ile His Gln Pro Glu Asn Pro Gln
116          420          425          430
118 His Phe Ala Cys Leu Leu Gly Arg Leu Thr Glu Leu Arg Thr Phe Asn
119          435          440          445
121 His His His Ala Glu Met Leu Met Ser Trp Arg Val Asn Asp His Lys
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129 <211> LENGTH: 472
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133 <400> SEQUENCE: 2
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137 Asp Glu Phe Ser Phe Ser Glu Asn Leu Phe Gly Val Leu Thr Glu Gln

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138          20          25          30
140 Val Ala Gly Pro Leu Gly Gln Asn Leu Glu Val Glu Pro Tyr Ser Gln
141          35          40          45
143 Tyr Ser Asn Val Gln Phe Pro Gln Val Gln Pro Gln Ile Ser Ser Ser
144          50          55          60
146 Ser Tyr Tyr Ser Asn Leu Gly Phe Tyr Pro Gln Gln Pro Glu Glu Trp
147 65          70          75          80
149 Tyr Ser Pro Gly Ile Tyr Glu Leu Arg Arg Met Pro Ala Glu Thr Leu
150          85          90          95
152 Tyr Gln Gly Glu Thr Glu Val Ala Glu Met Pro Val Thr Lys Lys Pro
153          100         105         110
155 Arg Met Gly Ala Ser Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val
156          115         120         125
158 Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys
159          130         135         140
161 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val
162 145          150          155          160
164 Tyr Lys Cys Lys Asn Gly Gly Asn Cys Val Met Asp Met Tyr Met Arg
165          165          170          175
167 Arg Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Lys Glu Met Gly Met
168          180         185         190
170 Leu Ala Glu Cys Leu Leu Thr Glu Ile Gln Cys Lys Ser Lys Arg Leu
171          195         200         205
173 Arg Lys Asn Val Lys Gln His Ala Asp Gln Thr Val Asn Glu Asp Ser
174          210         215         220
176 Glu Gly Arg Asp Leu Arg Gln Val Thr Ser Thr Thr Lys Ser Cys Arg
177 225          230          235          240
179 Glu Lys Thr Glu Leu Thr Pro Asp Gln Gln Thr Leu Leu His Phe Ile
180          245         250         255
182 Met Asp Ser Tyr Asn Lys Gln Arg Met Pro Gln Glu Ile Thr Asn Lys
183          260         265         270
185 Ile Leu Lys Glu Glu Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu Thr
186          275         280         285
188 Glu Met Ala Thr Asn His Val Gln Val Leu Val Glu Phe Thr Lys Lys
189          290         295         300
191 Leu Pro Gly Phe Gln Thr Leu Asp His Glu Asp Gln Ile Ala Leu Leu
192 305          310         315         320
194 Lys Gly Ser Ala Val Glu Ala Met Phe Leu Arg Ser Ala Glu Ile Phe
195          325         330         335
197 Asn Lys Lys Leu Pro Ser Gly His Ser Asp Leu Leu Glu Glu Arg Ile
198          340         345         350
200 Arg Asn Ser Gly Ile Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe
201          355         360         365
203 Tyr Lys Ser Ile Gly Glu Leu Lys Met Thr Gln Glu Glu Tyr Ala Leu
204          370         375         380
206 Leu Thr Ala Ile Val Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp
207 385          390         395         400
209 Arg Glu Ala Val Glu Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln
210          405         410         415

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212 Lys Leu Cys Lys Ile His Gln Pro Glu Asn Pro Gln His Phe Ala Cys
213           420           425           430
215 Leu Leu Gly Arg Leu Thr Glu Leu Arg Thr Phe Asn His His His Ala
216           435           440           445
218 Glu Met Leu Met Ser Trp Arg Val Asn Asp His Lys Phe Thr Pro Leu
219           450           455           460
221 Leu Cys Glu Ile Trp Asp Val Gln
222 465           470
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 229
227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens
230 <400> SEQUENCE: 3
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234 Tyr Asn Lys Gln Arg Met Pro Gln Glu Ile Thr Asn Lys Ile Leu Lys
235           20           25           30
237 Glu Glu Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu Thr Glu Met Ala
238           35           40           45
240 Thr Asn His Val Gln Val Leu Val Glu Phe Thr Lys Lys Leu Pro Gly
241           50           55           60
243 Phe Gln Thr Leu Asp His Glu Asp Gln Ile Ala Leu Leu Lys Gly Ser
244 65           70           75           80
246 Ala Val Glu Ala Met Phe Leu Arg Ser Ala Glu Ile Phe Asn Lys Lys
247           85           90           95
249 Leu Pro Ser Gly His Ser Asp Leu Leu Glu Glu Arg Ile Arg Asn Ser
250           100          105          110
252 Gly Ile Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe Tyr Lys Ser
253           115          120          125
255 Ile Gly Glu Leu Lys Met Thr Gln Glu Glu Tyr Ala Leu Leu Thr Ala
256           130          135          140
258 Ile Val Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp Arg Glu Ala
259 145          150          155          160
261 Val Glu Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln Lys Leu Cys
262           165          170          175
264 Lys Ile His Gln Pro Glu Asn Pro Gln His Phe Ala Cys Leu Leu Gly
265           180          185          190
267 Arg Leu Thr Glu Leu Arg Thr Phe Asn His His His Ala Glu Met Leu
268           195          200          205
270 Met Ser Trp Arg Val Asn Asp His Lys Phe Thr Pro Leu Leu Cys Glu
271           210          215          220
273 Ile Trp Asp Val Gln
274 225
277 <210> SEQ ID NO: 4
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279 <212> TYPE: PRT
280 <213> ORGANISM: Homo sapiens
282 <400> SEQUENCE: 4
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284      1              5              10              15
286 His His Lys Thr Tyr Asp Pro Thr Tyr Ser Asp Phe Cys Gln Phe Arg
287              20              25              30
289 Pro Pro Val Arg Val Asn Asp Gly Gly Gly Ser His Pro Ser Arg Pro
290              35              40              45
292 Asn Ser Arg His Thr Pro Ser Phe Ser Gly Asp Ser Ser Ser Ser Cys
293              50              55              60
295 Ser Asp His Cys Ile Thr Ser Ser Asp Met Met Asp Ser Ser Ser Phe
296 65              70              75              80
298 Ser Asn Leu Asp Leu Ser Glu Glu Asp Ser Asp Asp Pro Ser Val Thr
299              85              90              95
301 Leu Glu Leu Ser Gln Leu Ser Met Leu Pro His Leu Ala Asp Leu Val
302              100             105             110
304 Ser Tyr Ser Ile Gln Lys Val Ile Gly Phe Ala Lys Met Ile Pro Gly
305              115             120             125
307 Phe Arg Asp Leu Thr Ser Glu Asp Gln Ile Val Leu Leu Lys Ser Ser
308              130             135             140
310 Ala Ile Glu Val Ile Met Leu Arg Ser Asn Glu Ser Phe Thr Met Asp
311 145              150             155             160
313 Asp Met Ser Trp Thr Cys Gly Asn Gln Asp Tyr Lys Tyr Arg Val Ser
314              165             170             175
316 Asp Val Thr Lys Ala Gly His Ser Leu Glu Leu Ile Glu Pro Leu Ile
317              180             185             190
319 Lys Phe Gln Val Gly Leu Lys Lys Leu Asn Leu His Glu Glu Glu His
320              195             200             205
322 Val Leu Leu Met Ala Ile Cys Ile Val Ser Pro Asp Arg Pro Gly Val
323              210             215             220
325 Gln Asp Ala Ala Leu Ile Glu Ala Ile Gln Asp Arg Leu Ser Asn Thr
326 225             230             235             240
328 Leu Gln Thr Tyr Ile Arg Cys Arg His Pro Pro Pro Gly Ser His Leu
329              245             250             255
331 Leu Tyr Ala Lys Met Ile Gln Lys Leu Ala Asp Leu Arg Ser Leu Asn
332              260             265             270
334 Glu Glu His Ser Lys Gln Tyr Arg Cys Leu Ser Phe Gln Pro Glu Cys
335              275             280             285
337 Ser Met Lys Leu Thr Pro Leu Val Leu Glu Val Phe Gly Asn Glu Ile
338              290             295             300
340 Ser
341 305
344 <210> SEQ ID NO: 5
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346 <212> TYPE: PRT
347 <213> ORGANISM: Homo sapiens
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353 Gln Met Lys Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg
354              20              25              30
356 Leu Pro Gly Val Leu Ser Ser Gly Cys Glu Leu Pro Glu Ser Leu Gln

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VERIFICATION SUMMARY

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